

OIFE

CRF Errors Corrected by the STIC Systems Branch

Serial Number:

09/848,616

ENTERED

CRF Processing Date:

5/16/2001

Edited by:

Verified by: (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: *Seq 18 - moved base to left*

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING

DATE: 05/27/2001

PATENT APPLICATION: US/09/848,616

TIME: 17:48:05

Input Set : A:\Pto.amc

Output Set: C:\CRF3\05272001\I848616.raw

P.S

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4 <110> APPLICANT: Sebbel, Peter
5     Dunant, Nicolas
6     Bachmann, Martin
7     Tissot, Alain
8     Lechner, Franziska
10 <120> TITLE OF INVENTION: Molecular Antigen Array
13 <130> FILE REFERENCE: 1700.0180002
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/848,616
C--> 16 <141> CURRENT FILING DATE: 2001-05-05
18 <160> NUMBER OF SEQ ID NOS: 186
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 41
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Primer
30 <400> SEQUENCE: 1
31 ggggacgcgt gcagcaggta accaccgtta aagaaggcac c          41
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 44
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Primer
42 <400> SEQUENCE: 2
43 cggtggttac ctgctgcacg cggtgcttaa gcgacatgta gcgg      44
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 20
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Primer
54 <400> SEQUENCE: 3
55 ccatgaggcc tacgataccc          20
58 <210> SEQ ID NO: 4
59 <211> LENGTH: 25
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Primer
66 <400> SEQUENCE: 4
67 ggcactcacg gcgcgcttta caggc          25
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 47
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence

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75 <220> FEATURE:
76 <223> OTHER INFORMATION: Primer
78 <400> SEQUENCE: 5
79 ccttctttaa cggtggttac ctgctggcaa ccaacgtggt tcatgac 47
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 40
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Primer
90 <400> SEQUENCE: 6
91 aagcatgctg cacgcgtgtg cggtggtcgg atcgcccggc 40
94 <210> SEQ ID NO: 7
95 <211> LENGTH: 90
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Primer
102 <400> SEQUENCE: 7
103 gggctagat tcccaacat tcccttatcc aggctttttg acaacgctat gctccgcgcc 60
104 catcgtctgc accagctggc ctttgacacc 90
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 108
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Primer
115 <400> SEQUENCE: 8
116 gggctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60
117 gctggtttcg ctaccgtagc gcaggccttc ccaaccattc ctttatcc 108
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 31
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Primer
128 <400> SEQUENCE: 9
129 cccgaattcc tagaagccac agctgccctc c 31
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 24
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Primer
140 <400> SEQUENCE: 10
141 cctgcggtgg tctgaccgac accc 24
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 41
146 <212> TYPE: DNA

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147 <213> ORGANISM: Artificial Sequence
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150 <223> OTHER INFORMATION: Primer
152 <400> SEQUENCE: 11
153 ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g          41
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 33
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Primer
164 <400> SEQUENCE: 12
165 ctatcatcta gaatgaatag aggattcttt aac          33
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 15
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Modified ribosome
175      binding site
177 <400> SEQUENCE: 13
178 aggaggtaaa aaacg          15
181 <210> SEQ ID NO: 14
182 <211> LENGTH: 21
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: signal peptide
189 <400> SEQUENCE: 14
190 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
191   1           5           10           15
193 Thr Val Ala Gln Ala
194           20
197 <210> SEQ ID NO: 15
198 <211> LENGTH: 46
199 <212> TYPE: PRT
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: modified Fos
204      construct
206 <400> SEQUENCE: 15
207 Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
208   1           5           10           15
210 Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
211           20           25           30
213 Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
214           35           40           45
217 <210> SEQ ID NO: 16
218 <211> LENGTH: 6

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219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: peptide linker
225 <400> SEQUENCE: 16
226 Ala Ala Ala Ser Gly Gly
227   1           5
230 <210> SEQ ID NO: 17
231 <211> LENGTH: 6
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: peptide linker
238 <400> SEQUENCE: 17
239 Gly Gly Ser Ala Ala Ala
240   1           5
243 <210> SEQ ID NO: 18
244 <211> LENGTH: 256
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Fos fusion construct
251 <400> SEQUENCE: 18
252 gaattcagga ggtaaaaaac gatgaaaaag acagctatcg cgattgcagt ggcaactggct 60
253 ggtttcgcta ccgtagcgca ggcctgggtg ggggcggccg cttctggttg ttgcggtggt 120
254 ctgaccgaca cctgcaggc ggaaaccgac caggtggaag acgaaaaatc cgcgctgcaa 180
255 accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240
256 ggtggttgct aagctt                                     256
259 <210> SEQ ID NO: 19
260 <211> LENGTH: 52
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Fos fusion construct
267 <400> SEQUENCE: 19
268 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
269           5           10           15
271 Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
272           20           25           30
274 Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
275           35           40           45
277 His Gly Gly Cys
278           50
282 <210> SEQ ID NO: 20
283 <211> LENGTH: 261
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Fos fusion

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RAW SEQUENCE LISTING

DATE: 05/27/2001

PATENT APPLICATION: US/09/848,616

TIME: 17:48:05

Input Set : A:\Pto.amc

Output Set: C:\CRF3\05272001\I848616.raw

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289      construct
291 <220> FEATURE:
292 <221> NAME/KEY: CDS
293 <222> LOCATION: (22)..(240)
295 <400> SEQUENCE: 20
296 gaattcagga ggtaaaaaac g atg aaa aag aca gct atc gcg att gca gtg      51
297                               Met Lys Lys Thr Ala Ile Ala Ile Ala Val
298                               1           5           10
300 gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc      99
301 Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
302                               15           20           25
304 gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg      147
305 Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
306                               30           35           40
308 ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag      195
309 Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
310                               45           50           55
312 ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct      240
313 Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
314                               60           65           70
316 gggtgtgggg atatcaagct t      261
319 <210> SEQ ID NO: 21
320 <211> LENGTH: 73
321 <212> TYPE: PRT
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Fos fusion
326      construct
328 <400> SEQUENCE: 21
329 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
330 1           5           10           15
332 Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
333           20           25           30
335 Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
336           35           40           45
338 Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
339           50           55           60
341 Gly Gly Cys Gly Gly Ser Ala Ala Ala
342 65           70
346 <210> SEQ ID NO: 22
347 <211> LENGTH: 196
348 <212> TYPE: DNA
349 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
352 <223> OTHER INFORMATION: Fos fusion
353      construct
355 <220> FEATURE:
356 <221> NAME/KEY: CDS
357 <222> LOCATION: (34)..(189)

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/848,616

DATE: 05/27/2001

TIME: 17:48:06

Input Set : A:\Pto.amc

Output Set: C:\CRF3\05272001\I848616.raw

L:15 M:270 C: Current Application Number differs, Replaced Application Number

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:381 M:283 W: Missing Blank Line separator, <220> field identifier

L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111